SEQUENCE LISTING

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<120> CYTOCHROME C PROTEIN AND ASSAY

<130> PA0394

<140> TO BE ASSIGNED
<141> 2006-06-19

<150> PCT/GB2004/005317
<151> 2004-12-17

<150> GB 0329353.7
<151> 2003-12-19

<160> 15

<170> PatentIn version 3.3

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<212> DNA
<213> Homo sapiens

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acaggtcagg cccctggata ctcttacaca gccgccaata agaacaaagg catcatctgg 180

ggagaggata cactgatgga gtatttggag aatcccaaga agtacatccc tggaacaaaa 240

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<210> 2
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<213> Homo sapiens

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Gln Cys His Thr Val Glu Lys Gly Gly Lys His Lys Thr Gly Pro Asn
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Leu His Gly Leu Phe Gly Arg Lys Thr Gly Gln Ala Pro Gly Tyr Ser
35 40 45

Tyr Thr Ala Ala Asn Lys Asn Lys Gly Ile Ile Trp Gly Glu Asp Thr
50 55 60

Leu Met Glu Tyr Leu Glu Asn Pro Lys Lys Tyr Ile Pro Gly Thr Lys
65 70 75 80

Met Ile Phe Val Gly Ile Lys Lys Lys Glu Glu Arg Ala Asp Leu Ile
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Ala Tyr Leu Lys Lys Ala Thr Asn Glu
100 105

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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

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aaacttaccc ttaaatttat ttgcactact ggaaaactac ctgttccatg gccaacactt 180

gtcactactc tctcttatgg tgttcaatgc ttttcaagat acccagatca tatgaaacgg 240

catgactttt tcaagagtgc catgcccgaa ggttatgtac aggaaagaac tatatttttc 300

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ttggaataca actataactc acacaatgta tacatcatgg cagacaaaca aaagaatgga 480

atcaaagtta acttcaaaat tagacacaac attgaagatg gaggcgttca actagcagac 540

cattatcaac aaaatactcc aattggcgat ggccctgtcc ttttaccaga caaccattac 600

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<212> PRT
<213> Artificial Sequence

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<223> Synthetic polypeptide

<400> 4

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Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
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Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
    50                  55                  60

Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130                 135                 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145                 150                 155                 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val
                165                 170                 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
            180                 185                 190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
        195                 200                 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Gly Phe Val
    210                 215                 220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys Leu Glu
225                 230                 235                 240

Asn Ser Thr Met Gly Asp Val Glu Lys Gly Lys Lys Ile Phe Ile Met
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245 250 255

Lys Cys Ser Gln Cys His Thr Val Glu Lys Gly Gly Lys His Lys Thr
260 265 270

Gly Pro Asn Leu His Gly Leu Phe Gly Arg Lys Thr Gly Gln Ala Pro
275 280 285

Gly Tyr Ser Tyr Thr Ala Ala Asn Lys Asn Lys Gly Ile Ile Trp Gly
290 295 300

Glu Asp Thr Leu Met Glu Tyr Leu Glu Asn Pro Ala Lys Tyr Ile Pro
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Gly Thr Lys Met Ile Phe Val Gly Ile Lys Lys Lys Glu Glu Arg Ala
325 330 335

Asp Leu Ile Ala Tyr Leu Lys Lys Ala Thr Asn Glu
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acaggtcagg cccctggata ctcttacaca gccgccaata agaacaaagg catcatctgg 180

ggagaggata cactgatgga gtatttggag aatcccgcca agtacatccc tggaacaaaa 240

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gtcccaattc ttgttgaatt agatggtgat gttaatgggc acaaattttc tgtcagtgga 420

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tcaagatacc cagatcatat gaaacggcat gacttttttca agagtgccat gcccgaaggt 600

tatgtacagg aaagaactat atttttcaaa gatgacggga actacaagac acgtgctgaa 660

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gaagatggaa acattcttgg acacaaattg gaatacaact ataactcaca caatgtatac 780

atcatggcag acaaacaaaa gaatggaatc aaagttaact tcaaaattag acacaacatt 840

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cctgtccttt taccagacaa ccattacctg tccacacaat ctgccctttc gaaagatccc 960

aacgaaaaga gagaccacat ggtccttctt ggctttgtaa cagctgctgg gattacacat 1020

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<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic polypeptide

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Gln Cys His Thr Val Glu Lys Gly Gly Lys His Lys Thr Gly Pro Asn
20 25 30

Leu His Gly Leu Phe Gly Arg Lys Thr Gly Gln Ala Pro Gly Tyr Ser
35 40 45

Tyr Thr Ala Ala Asn Lys Asn Lys Gly Ile Ile Trp Gly Glu Asp Thr
50 55 60

Leu Met Glu Tyr Leu Glu Asn Pro Ala Lys Tyr Ile Pro Gly Thr Lys
65 70 75 80

Met Ile Phe Val Gly Ile Lys Lys Lys Glu Glu Arg Ala Asp Leu Ile
85 90 95

Ala Tyr Leu Lys Lys Ala Thr Asn Glu Gly Arg Pro Gly Met Ser Lys
100 105 110

Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp
115 120 125

Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly
130 135 140

Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly
145 150 155 160

Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Ser Tyr Gly
165 170 175

Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg His Asp Phe
180 185 190

Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe
195 200 205

Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu
210 215 220

Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys
225 230 235 240

Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser
245 250 255

His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val
260 265 270

Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala
275 280 285

Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
290 295 300

Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
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Asn Glu Lys Arg Asp His Met Val Leu Leu Gly Phe Val Thr Ala Ala
325 330 335

Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
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aaacttaccc ttaaatttat ttgcactact ggaaaactac ctgttccatg gccaacactt 180

gtcactactc tctcttatgg tgttcaatgc ttttcaagat acccagatca tatgaaacgg 240

catgactttt tcaagagtgc catgcccgaa ggttatgtac aggaaagaac tatatttttc 300

aaagatgacg ggaactacaa gacacgtgct gaagtcaagt ttgaaggtga tacccttgtt 360

aatagaatcg agttaaaagg tattgatttt aaagaagatg gaaacattct tggacacaaa 420

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<220>
<223> Synthetic polypeptide

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Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
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Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35                  40                  45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
    50                  55                  60

Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg
65                  70                  75                  80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85                  90                  95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100                 105                 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115                 120                 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
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130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Gly Phe Val
210 215 220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys Leu Glu
225 230 235 240

Asn Ser Thr Met Gly Asp Val Glu Lys Gly Lys Lys Ile Phe Ile Met
245 250 255

Lys Cys Ser Gln Cys His Thr Val Glu Lys Gly Gly Lys His Lys Thr
260 265 270

Gly Pro Asn Leu His Gly Leu Phe Gly Arg Lys Thr Gly Gln Ala Pro
275 280 285

Gly Tyr Ser Tyr Thr Ala Ala Asn Lys Asn Lys Gly Ile Ile Trp Gly
290 295 300

Glu Asp Thr Leu Met Glu Tyr Leu Glu Asn Pro Lys Lys Tyr Ile Pro
305 310 315 320

Gly Thr Lys Met Ile Phe Val Gly Ile Lys Lys Lys Glu Glu Arg Ala
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Asp Leu Ile Ala Tyr Leu Lys Lys Ala Thr Asn Glu
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<210> 9
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<212> DNA
<213> Artificial Sequence

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ggagaggata cactgatgga gtatttggag aatcccaaga agtacatccc tggaacaaaa    240
atgatctttg tcggcattaa gaagaaggaa gaaagggcag acttaatagc ttatctcaaa    300
aaagctacta atgagggtcg acccgggatg agtaaaggag aagaactttt cactggagtt    360
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gaagatggaa acattcttgg acacaaattg gaatacaact ataactcaca caatgtatac    780
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Gln Cys His Thr Val Glu Lys Gly Gly Lys His Lys Thr Gly Pro Asn
            20                  25                  30

Leu His Gly Leu Phe Gly Arg Lys Thr Gly Gln Ala Pro Gly Tyr Ser
        35                  40                  45

Tyr Thr Ala Ala Asn Lys Asn Lys Gly Ile Ile Trp Gly Glu Asp Thr
    50                  55                  60

Leu Met Glu Tyr Leu Glu Asn Pro Lys Lys Tyr Ile Pro Gly Thr Lys
65                  70                  75                  80
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Met Ile Phe Val Gly Ile Lys Lys Lys Glu Glu Arg Ala Asp Leu Ile
85 90 95

Ala Tyr Leu Lys Lys Ala Thr Asn Glu Gly Arg Pro Gly Met Ser Lys
100 105 110

Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp
115 120 125

Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly
130 135 140

Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly
145 150 155 160

Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Ser Tyr Gly
165 170 175

Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg His Asp Phe
180 185 190

Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe
195 200 205

Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu
210 215 220

Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys
225 230 235 240

Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser
245 250 255

His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val
260 265 270

Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val Gln Leu Ala
275 280 285

Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
290 295 300

Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
305 310 315 320

Asn Glu Lys Arg Asp His Met Val Leu Leu Gly Phe Val Thr Ala Ala
325 330 335

Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
340 345

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